

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 27, 2001, 13:07:57 ; Search time 2039.32 Seconds
(without alignments)
12788.784 Million cell updates/sec

Title: US-09-784-340-1
Perfect score: 2759

Sequence: 1 caaccattgcagatcagtg.....ctgcagccgtctacgtacgc 2759

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 10228115 seqs, 4726426750 residues

Word size : 0

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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ESP:*
1: gb_est1:*
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257: gb_est188:*
258: gb_est189:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT	4
BG402144	
LOCUS	BG402144 898 bp mRNA EST 12-MAR-2001
DEFINITION	602465689P1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4593694 5' , mRNA sequence.
ACCESSION	BG402144
VERSION	BG402144.1 GI:1329592
KEYWORDS	EST .
SOURCE	human .
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo .

REFERENCE 1 (bases 1 to 898)
 AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Clontech Laboratories, Inc.
 CDNA Library Preparation: Clontech Laboratories, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
 Plate: LICM1334 row: a column: 23
 High quality sequence stop: 557.

FEATURES

source

1. 898
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4593694"
 /clone_1ib="NIH-MGC-75"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: Kidney; Vector: pDNR-LIB (Clontech); site_1: SfiI (ggcgctcgcc); site_2: SfiI (ggcattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGGCGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH-MGC Library."

BASE COUNT 249 a 175 c 165 g 309 t
 ORIGIN

Query Match 8.5%; Score 234; DB 153; Length 898;
 Best Local Similarity 99.6%; Pred. No. 3.2e-104;
 Matches 284; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1508 gtagatggtctcgtcgtgacctgtgtgcaactgctatcttctgtccacaatgtttc 1567
 Db 1 GTGATTTGGTCTCGTCCGTGACCTGTGTGGCAACTGCTATTCTTGTTCACAAAATGTTTT 60
 QY 1568 ttatttcctgtcaaaaatttaaaactagaagaatagaagaaggaatagatttt 1627
 Db 61 TTATTTTCCGTCAAAATTAATTAAGTAGAAGAGAGAGGAGATGATCTTT 120
 QY 1628 ccaaatcaagaagacctatggtggaatccctgttaattccaccacaatgaattggt 1687
 Db 121 CCAAAATCAAGAAAGACCTGATGGGTAAATCCTGTAAATTCACGCCACATAGAAATTGGT 180
 QY 1688 gaaaacctgctatttcataataatactatctcgttatttatttactttagatagcctag 1747
 Db 181 GGAACCTGCTATTTCATATTAATCTATCTGTTATTTATTTACTATATAGAGCTAG 240
 QY 1748 aattcatgcatgaggtgtgtgagatatcatcttcttcgttg 1792
 Db 241 AATTCATGATCATGAGGTGTGTGATATATCTCATCTCTTCGTTG 285

RESULT 5

AO165734

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AO165734 367 bp DNA GSS 16-OCT-1998
 HS-3065_B1_H05_MR_C1T Approved Human Genomic Sperm Library D Homo
 sapiens genomic clone Plate=3065 COL-9 Row=P, DNA sequence.
 AO165734.1 GI:3563929
 GSS.
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 367)
 AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
 Hood,L.
 TITLE Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
 MEDLINE 99380589
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Sequence Tagged Connector
 Plate: 3065 row: P column: 9
 Class: BAC ends
 High quality sequence stop: 367.

FEATURES

source

1. 367
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="Plate=3065 COL-9 Row=P"
 /clone_1ib="C1T Approved Human Genomic Sperm Library D"
 /sex="male"
 /note="Organ: sperm; Vector: pBel0BAC11; BAC Clones in E-Coll DH10B"

BASE COUNT 113 a 74 c 50 g 130 t
 ORIGIN

Query Match 8.3%; Score 229; DB 225; Length 367;
 Best Local Similarity 99.6%; Pred. No. 9e-102;
 Matches 279; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1794 atttctcaggtgtgcttactcttcttctcacttgtgtgacacaggaacatgaatcac 1853
 Db 42 ATTTTCCTAGGTGTGCTTACTCTCTCTCCTCCTCCTGACACAGGACATGATATCATC 101
 QY 1854 taatttccattctcgatataactgttccatgaagctattctctcacttaag 1913
 Db 102 TAAATTTTCCATTTCGATATCACTGTTCCACAGGCTCATTTCTTCAACCTTAAG 161
 QY 1914 tgataggttaccctgaatgctgattcctgtgtgttgcacaaacatgagatgaag 1973
 Db 162 TGATAGGCTGACCTGCATATGCTGATTCCTGGTGTTCACAAACACATGATGTAAG 221
 QY 1974 aagtaaaaatgtlaaaattcacaattcagtaaacacacacaatcaatgaagcatc 2033
 Db 222 AAGTAAATAATGTAAATTTCAAAATTCAGTATACCAACAAATCAATGAAGCATCTA 281
 QY 2034 tgacattagcttgttatgagtaacataagatttcttc 2073
 Db 282 TGACATTAGCTTGTATGAGTAACATATGATTTTCTT 321

RESULT 6

AO784447

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AO784447 595 bp DNA GSS 03-AUG-1999
 HS-3141_A2_H04_T7C C1T Approved Human Genomic Sperm Library D Homo
 sapiens genomic clone Plate=3141 COL-# Row=O, DNA sequence.
 AO784447.1 GI:5692071
 GSS.
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
 Hood,L.

TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL	Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE	99380589
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L

BASE COUNT ORIGIN	186 a	115 c	87 g	200 t	7 others
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Query Match	7.5%	Score 206;	DB 233;	Length 595;
Best Local Similarity	100.0%	Pred. No. 2.1e-90;		
Matches 206; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

QY	1868	tcgataccacgttccacaagcatcactctcctaaccctaaagtgtgaagtgacct	1927
Db	133	TCGATATCACTGTTTCACATGACGACTTACTTCTCTAACCTTAAGTAGAGGACT	192
QY	1928	gcacataatgcgatctctgtgtgtttgcacaaacacatgatatgaagaagtataaaatgta	1987
Db	193	GCAATATAGCTGATCTCCGCGGTTTGCACCAACACATGAGTGTGTAAGAACTATAAAATGTGA	252

QY	2048	tatgagtaacataatgattttttttc	2073
QY	1988	aaattcccaaaatttcgtaaacacacacaaatcaatgaaacatttcatagacataactgt	2047
Db	253	AAATTCCAAAATTTCAGTAAACACACACAAATCAATGAACATTTCATATGACATTACTTGT	312

RESULT	7
LOCUS	B80712
DEFINITION	B80712 444 bp DNA GSS 24-OCT-1998 CIT-HSP-2050M23.TR CIT-HSP Homo sapiens genomic clone 2050M23, DNAA
ACCESSION	B80712
VERSION	B80712.1 GI:2867735
KEYWORDS	GSS.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 444)
AUTHORS	Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Sun,E., Wible,C., Shizuya,H., Simon,M., and Venter,J.C. Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998) Unpublished (1998) Other_GSSs: CIT-HSP-2050M23.TR
TITLE	Contact: Mark Adams
JOURNAL	Department of Eukaryotic Genomics
COMMENT	

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel.: 301 838 0200
Tel.: 301 838 0208
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M3-21
Class: BAC ends.

```

/ote="Vector: pbeloBAC11; Site_1: HindII; Site_2:
HindII"
BASE COUNT      124 a      71 g      139 t
ORIGIN

```

Query Match	5.7%;	Score 158;	DB 257;	Length 444;
Best Local Similarity	100.0%;	Pred. No. 1.1e-66;		
Matches 158;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

[illegible]

RESULT	8
LOCUS	A0728754/c
DEFINITION	A0728754 474 bp DNA GSS 15-JUL-1999
ACCESSION	H5_5462_B1-E10.SP6E Rcpc1-11 Human Male BAC Library Homo sapiens
VERSION	genomic clone Plate=1038 Col=19 Row=C, DNA sequence.
KEYWORDS	A0728754 A0728754.1 GI:5500306
SOURCE	GSS.
ORGANISM	human.
REFERENCE	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 474) Mahairas,G.G., Wallace,J.C., Smith,R., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL	Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE	99380589
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel.: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Clones are derived from the human BAC library Rcpc1-11. For BAC library availability, please contact pietre de Jong (pietredejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)

or from Resear h Genetics (info@resgen.com). BAC end Web Server:
<http://www.htsc.washington.edu>
 Plate: 1038 row: J column: 19
 Seq primer: SP6
 Class: BAC ends
 High quality sequence stop: 474.
 Location/Qualifiers

FEATURES

source

1. 474
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="Plate-1038 Col-19 Row-J"
 /clone_lib="RPCI-11 Human Male BAC Library"
 /sex="male"
 /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
 Male blood DNA was isolated from one randomly chosen donor
 and partially digested with a combination of EcoRI and
 EcoRI Methylase. Size selected DNA was cloned into the
 pBAC3.6 vector at EcoRI sites"
 BASE COUNT 146 a 90 c 90 g 143 t 5 others
 ORIGIN

Query Match 5.1%; Score 142; DB 232; Length 474;
 Best Local Similarity 100.0%; Pred. No. 8.4e-59;
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1588 taataaacagagaataaagaggagatagatcttcacaaattcagaagacctg 1647
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 159 TAAATAAAGCTAGAAAGATGAAAGAGGGAATGATCTTCCAAATTCAGAAAGACCTG 100
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 1648 atggggtaactcgttaattccagccacatagattgtgtaaaccttctattcat 1707
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 99 ATGGGTAATCCGTAAATCCAGCCACATAGATTGTGGAACCTCTCTATTTCAT 40
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 1708 attatctattctgtatttat 1729
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 39 ATTATCTATTTCTGTATTATTTAT 18
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 9
 LOCUS AO3711717 601 bp DNA GSS 20-MAY-1999
 DEFINITION RPC111-155J15, TV RPCI-11 Homo sapiens genomic clone RPCI-11-155J15,
 DNA sequence.
 ACCESSION AO3711717
 VERSION AO3711717.1 GI:4342740
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 601)
 AUTHORS Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter,
 J.C.
 TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
 Map Building
 JOURNAL Unpublished (1997)
 COMMENT Other_GSSs: RPC111-155J15.TV
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@edj.med.buflalo.edu). Clones may be purchased from
 BAC2C Resources (<http://bacpac.med.buflalo.edu/ordering>) or from
 Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/cdb/humgen/Bac_end_search/Bac_end_search.html
 Seq primer: 17
 Class: BAC ends.

FEATURES
 Location/Qualifiers

source

1. 601
 /organism="Homo sapiens"
 /db_xref="GBD:7559366"
 /db_xref="taxon:9606"
 /clone="RPCI-11-155J15"
 /clone_lib="RPCI-11"
 /sex="Male"
 /cell_type="lymphocytes"
 /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
 RPCI11 Human Male BAC Library"
 BASE COUNT 227 a 89 c 85 g 200 t
 ORIGIN

Query Match 4.8%; Score 132; DB 227; Length 601;
 Best Local Similarity 100.0%; Pred. No. 7.3e-54;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 622 tatgacagactaacagacagatgacctctctggaagagtaaaaaatcaatgcttc 681
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 553 TATGACAGGACTTAACAGACAGATGACCTTCTGGAAGATAAAAATCAATGCTTTC 494
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 682 agttgttccactctgtgattcagattacgacatcatcttttgggaagatttatag 741
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 493 AGTTTCTTCACCTCTGTGATTCAGATTCAGACTATCATTTTGGGAGAGTTTATAG 434
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 OY 742 taaggcattagg 753
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 433 TAAGGCATTAGG 422
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 10
 LOCUS AM301261 536 bp mRNA EST 18-JAN-2000
 DEFINITION xs69g08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2774942 3',
 mRNA sequence.
 ACCESSION AM301261
 VERSION AM301261.1 GI:6710938
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 536)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Christopher Moskalkuk, M.D., Ph.D., Michael R.
 Emmerit-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at:
www.bio.livl.gov/bdrp/image/image.html
 Seq primer: -40UP from Glibco
 High quality sequence stop: 461.
 Location/Qualifiers

FEATURES
 source

1. 536
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2774942"
 /clone_lib="NCI_CGAP_Kid11"
 /lab_host="DH10B"
 /note="Organ: Kidney; Vector: p773D-Pac (Pharmacia) with
 a modified polylinker; Site_1: Not I; Site_2: Eco RI;
 Plasmid DNA from the normalized library NCI_CGAP_Kid3 was
 prepared, and ss circles were made in vitro. Following HAP
 purification, this DNA was used as tracer in a subtractive

hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonids 132376-132391, 145607-145675, and 150052-150285). Subtraction by Bento Soares and M. Fatima Bonaldo.

BASE COUNT 214 a 62 c 52 g 208 t

Query Match 3.2%; Score 88; DB 114; Length 536;
Best Local Similarity 100.0%; Pred. No. 3.9e-32;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2449 aaatgatgaatactcataatcttctctataatcaaaagataattactgtaga 2508
|||||
DB 518 AAATGATGAACTCATTAATCTTCTTAATCAAAAGTAAATTACTGTAGAAA 459
OY 2509 aataagagatgctgtcttctgaagtaa 2536
|||||
DB 458 AATAAGAGAGATGCTTGTCTGAAAGTAA 431

RESULT 11
AI816782/c 552 bp mRNA EST 21-DEC-1999
LOCUS wj34a11.x1 NCI_CGAP_Kid12 Homo sapiens cDNA IMAGE:2404700 3',
DEFINITION mRNA sequence.
ACCESSION AI816782
VERSION AI816782.1 GI:5435861
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 552)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gene Index
Tumor Gene Index
Unpublished (1997)
CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-dio.llnl.gov/dbirp/image/image.html
Insert length: 1622 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 450.
Location/Qualifiers

FEATURES
source
1..552
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2404700"
/clone_lib="NCI-CGAP_Kid12"
/tissue_type="2-pooled tumors (clear cell type)"
/lab_host="DH10B"
/note="Organ: Kidney; Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonids 1323912-1325831, 1471368-1472903 and 1492104-1493255). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 215 a 65 c 52 g 220 t

Query Match 3.2%; Score 88; DB 102; Length 552;
Best Local Similarity 100.0%; Pred. No. 3.9e-32;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2449 aaatgatgaatactcataatcttctctataatcaaaagataattactgtaga 2508
|||||
DB 527 AAATGATGAACTCATTAATCTTCTTAATCAAAAGTAAATTACTGTAGAAA 468
OY 2509 aataagagatgctgtcttctgaagtaa 2536
|||||
DB 467 AATAAGAGAGATGCTTGTCTGAAAGTAA 440

RESULT 12
AW771510/c 498 bp mRNA EST 04-MAY-2000
LOCUS hm57e11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3032012 3',
DEFINITION mRNA sequence.
ACCESSION AW771510
VERSION AW771510.1 GI:7703567
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 498)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gene Index
Tumor Gene Index
Unpublished (1997)
CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 459.
Location/Qualifiers

FEATURES
source
1..498
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3032012"
/clone_lib="NCI_CGAP_Kid11"
/lab_host="DH10B"
/note="Organ: Kidney; Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonids 132376-132391, 145607-145675, and 150052-150285). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 191 a 58 c 50 g 199 t

Query Match 3.2%; Score 87; DB 120; Length 498;
Best Local Similarity 100.0%; Pred. No. 1.2e-31;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2450 aaatgatgaatactcataatcttctctataatcaaaagataattactgtaga 2509
|||||
DB 498 AAATGATGAACTCATTAATCTTCTTAATCAAAAGTAAATTACTGTAGAAA 439
OY 2510 aataagagatgctgtcttctgaagtaa 2536

Db 438 ATAAAGAGATGCTTGTCTGAAGTAA 412

RESULT 13
LOCUS A1670866/c 518 bp mRNA EST 16-DEC-1999
DEFINITION wa05b11.x1 NCI-CGAP_Kid11 Homo sapiens cDNA clone IMAGE:229727 3',
mRNA sequence.
ACCESSION A1670866
VERSION A1670866
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 518)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabp@remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/dbip/image/image.html
Insert Length: 1265 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 457.
Location/Qualifiers
1. 518
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:229727"
/clone_1ib="NCI-CGAP_Kid11"
/lab_host="DH10B"
/note="Organ: kidney; Vector: pT730-Pac (Pharmacia) with
a modified polylinker; Site.1: Not I; Site.2: Eco RI;
Plasmid DNA from the normalized library NCI-CGAP Kid3
prepared, and as circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneids 1322376-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo."

BASE COUNT 203 a 61 c 54 g 200 t

ORIGIN

Query Match 3.1%; Score 85; DB 23; Length 518;
Best Local Similarity 100.0%; Pred. No. 1.2e-30;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2452 atgataactcataattctatctcacaagaataattactgtagaanaat 2511
|||||
DB 518 ATGATGATACATCATATCTTATCTCTATTAACAAAGATATATTACTGTGAANAAT 459
|||||
QY 2512 aaagagatgctgttctgaagtaa 2536
|||||
DB 458 AAAGAGATGCTGTCTGAAGTAA 434

RESULT 14
LOCUS BF132129 538 bp mRNA EST 24-OCT-2000
DEFINITION 601821157F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052654 5',
mRNA sequence.

ACCESSION BF132129
VERSION BF132129.1 GI:10971169
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 538)
AUTHORS NIH-MGC <http://imgc.ncbi.nlm.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabp@remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L1CM890 row: b column: 15
High quality sequence stop: 536.
Location/Qualifiers
1. 538
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4052654"
/clone_1ib="NIH_MGC_58"
/tissue_type="hypernephroma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pNR-LIB (Clontech); Site.1:
SfiI (ggcgctcgcc); Site.2: SfiI (ggcgctcgcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-ATTCTAGAGCGCGCGCCGACATG-dt(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.35 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."

BASE COUNT 172 a 103 c 118 g 145 t

ORIGIN

Query Match 2.6%; Score 73; DB 144; Length 538;
Best Local Similarity 100.0%; Pred. No. 1e-24;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1062 catccacattagagccaactcggctgatattgatacccgagaatgactcttg 1121
|||||
DB 450 CATCCACATTAGAGCCCAATACATCGCTGATATGATGATGCCAGAAATGATCTCTTG 509
|||||
QY 1122 gtcatcccaaac 1134
|||||
DB 510 GTCATCCCAAAAC 522

RESULT 15
LOCUS AQ438194 552 bp DNA GSS 31-MAR-1999
DEFINITION HS.5083.B2.E12.T7A RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate-659 Col-24 Row-J, DNA sequence.
ACCESSION AQ438194
VERSION AQ438194.1 GI:4549533
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 552)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and

TITLE Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
 MEDLINE 99380589
 COMMENT Contact: Mahalras GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCT-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
 or from Research Genetics (info@resgen.com). BAC end Web Server:
<http://www.htsc.washington.edu>
 Plate: 659 row: J column: 24

Seq primer: T7
 Class: BAC ends
 High quality sequence stop: 552.

FEATURES

source location/Qualifiers
 1..552
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="Plate=659 Col=24 Row=J"
 /clone_lib="RPCT-11 Human Male BAC Library"
 /sex="male"
 /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
 Male blood DNA was isolated from one randomly chosen donor
 and partially digested with a combination of EcoRI and
 EcoRI Methylase. Size selected DNA was cloned into the
 pBACe3.6 vector at EcoRI sites"
 BASE COUNT 172 a 111 c 84 g 181 t 4 others
 ORIGIN

Query Match 2.6%; Score 72; DB 228; Length 552;
 Best Local Similarity 100.0%; Pred. No. 3.1e-24;

Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2071 |tttcaatttaataagcccttaccatccccagcatctgactcagacaatgaatt 2130
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 333 TTTTCAATTTAATAAGCCCTTACATACCCAGCATTCGATCTCAGACATGAT 392

QY 2131 |gtataaaatgac 2142
 ||||||||||||
 DB 393 GCTAATAATGAC 404

Search completed: August 27, 2001, 14:22:51
 Job time: 4494 sec